

WHAT IS CLAIMED IS:

1. A method for examining a gene comprising detecting a variation in nucleic-acid bases in at least two or more positions within a gene region containing a glaucoma-related gene coding region and/or an upstream region and predicting any future development of glaucoma using said variation as an index.
2. The method according to Claim 1 wherein the glaucoma-related gene is a myocilin (MYOC) gene.
3. The method according to Claim 1 or 2 wherein the gene region is the nucleic-acid base sequence represented by SEQ ID No: 1.
4. The method according to any one of Claims 1 to 3 wherein the variation in a base is a substitution, deletion and/or insertion.
5. The method according to Claim 3 which detects any of the group consisting of, in the nucleic-acid base sequence represented by SEQ ID No: 1, the C-to-A substitution at position 194; the A-to-C substitution at position 199; the G-to-A substitution at position 324; the C-to-T substitution at position 1051; the C-to-T substitution at position 1084; the T-to-C substitution at position 1627; the T-to-C substitution at position 1685; the C-to-T substitution at position 1756; the G-to-C substitution at position 1853; the G-to-A substitution at position 2830; the A-to-G substitution at position 3371; the G-to-A substitution at position 4037; and the G-to-A substitution at position 4346.
6. The method according to Claim 3 which detects at least two or more simultaneous substitutions selected from the group consisting of, in the nucleic-acid base sequence represented by SEQ ID No: 1, the C-to-A substitution at position 194; the C-to-T substitution at position 1084; the T-to-C substitution at position 1627; the G-to-A substitution at position 4037; and the G-to-A substitution

at position 4346.

7. The method according to Claim 3 which detects at least two or more simultaneous substitutions selected from the group consisting of, in the nucleic-acid base sequence represented by SEQ ID No: 1, the C-to-T substitution at position 1051; the T-to-C substitution at position 1685; the C-to-T substitution at position 1756; and the G-to-C substitution at position 1853.

8. A method for examining a gene comprising detecting at least one substitution of the group consisting of, in the nucleic-acid base sequence represented by SEQ ID No: 1, the A-to-C substitution at position 199; the G-to-A substitution at position 324; the C-to-T substitution at position 1051; the C-to-T substitution at position 1084; the T-to-C substitution at position 1627; the T-to-C substitution at position 1685; the C-to-T substitution at position 1756; the G-to-C substitution at position 1853; the G-to-A substitution at position 2830; and the A-to-G substitution at position 3371 and predicting any future development of glaucoma using said variation as an index.

9. The method according to any one of Claims 1 to 8 wherein the glaucoma is primary open-angle glaucoma and/or normal tension glaucoma.

10. The method according to any one of Claims 1 to 9 wherein the variation is detected using an oligonucleotide capable of specifically forming a hybrid with a part of a gene region containing a glaucoma-related gene coding region and/or an upstream region.

11. A primer function-possessing oligonucleotide wherein the oligonucleotide, which is capable of specifically forming a hybrid with a part of a gene region containing a glaucoma-related gene coding region and/or an upstream region, is at least one or more selected from the group consisting of:

1) an oligonucleotide consisting of a nucleic-acid base sequence represented by any of SEQ ID Nos. 2 to 27;

2) a strand complementary with the oligonucleotide according to the above-mentioned 1);

3) an oligonucleotide capable of hybridizing under a stringent condition with the oligonucleotide according to the above-mentioned 1) or 2);

4) an oligonucleotide having a homology of about 60% with the oligonucleotide according to any one of the above-mentioned 1) to 3);

5) an oligonucleotide having a nucleic-acid base sequence whose 1 or more base of oligonucleotides according to the above-mentioned 1) to 4) was subjected to a variation such as a substitution, deletion, insertion or addition.

12. The method according to any one of Claims 1 to 9 comprising performing a nucleic acid amplification process using at least one oligonucleotide selected from the oligonucleotides according to Claim 11.

13. An examination reagent or examination reagent kit comprising a reagent employed in the examination method according to any one of Claims 1 to 10 or Claim 12.